Novel high-throughput single cell analytical methods using Particle-templated Instant Partitions (PIPseq[™])

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Introduction: Single cell transcriptomics has revolutionized modern biology by providing unprecedented insight into the mechanisms of cellular differentiation and function in complex tissues and organisms. As scRNA-seq transitions from a discovery tool into broader translational applications requiring complex experimental design and flexibility, there is a growing need for simple, scalable, and cost-effective library preparation methods. Fluent BioSciences has developed new methods for scRNA-seq enabled by Particle-templated Instant Partitions (PIPseq), for simple, sensitive, and scalable scRNA-seq. We demonstrate single-tube PIPseq configurations accommodating from 2,000 to over 100,000 cells and evaluate key performance metrics using model cell lines, peripheral blood mononuclear cells (PBMCs), and complex tissues.

Materials and Methods: Fluent BioSciences 3' Single Cell RNA Kits (T2, T20 and T100) were used to profile a range of sample types including human breast tissue composition from reduction mammoplasty patients, fresh mouse brain cells and PBMCs. UMAP analyses of the transcriptome were performed and compared against data generated from the 10x Genomics platform (for mouse brain).

Results: We demonstrate that major cell types were clearly annotated based on known marker genes and differential gene expression analysis revealed comparable cell populations between PIPseq and 10x datasets.

Conclusion: PIPseq is an intrinsically scalable, effective, and affordable solution for single-cell analysis that can be implemented in any laboratory. PIPseq reagent kits scaled for 2,000, 20,000 and 100,000 cell capture provide new capabilities for single-cell analysis in research, clinical, and translational applications and eliminate barriers to accessibility, enabling single-cell analysis in any laboratory.